

WO 00/11159

PCT/BE99/00112

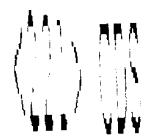
1

SEQUENCE LISTING

<110> CATHOLIC UNIVERSITY OF LOUVAIN

<120> PHARMACEUTICAL COMPOSITION INTENDED FOR THE TREATMENT OR
PREVENTION OF DIABETES OR OF CANCER

5



<212> DNA
<213> *Homo sapiens*

2007-08
2008-09
2009-10

366

170

176

1364

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 Gin Glu Pro Glu Phe Gin Arg Met Ser Ala Leu Arg Leu Ala Cys
 380 385 390

aaa cgt aaa caq cca cca aac aaa ccc aag aac aat tcc caq aag
 Lys Arg Lys Glu Gin Glu Pro Asn Lys Asp Arg Asn Asn Ser Gin Lys
 395 400 405

aag tcc ccc ccc gtc ttc act ccc ccc ccc aca aca ccc tcc gcc
 Lys Ser Arg Leu Val Phe Thr Asp Leu Gin Arg Arg Thr Leu Phe Ala
 410 415 420

atc tcc aag caq aac aaa ccc ccc tca aag gag atc aag atc acc att
 Ile Phe Lys Glu Asn Lys Arg Pro Ser Lys Glu Met Gin Ile Thr Ile
 425 430 440

atc caq caq ccc ccc gag atc aca acc gtc aac tcc tcc atc
 Ala Gin Gin Leu Glu Leu Gin Leu Thr Val Ser Asn Phe Phe Met
 445 450

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 Asn Ala Arg Arg Ser Ser Leu Glu Lys Tyr Gin Asp Asp Leu Ser Thr
 460 465 470

ccc ccc tcc tcc acc tcc acc acc tcc acc aaa cca tgcggaaagg
 Gly Gly Ser Ser Ser Thr Ser Thr Cys Thr Lys Ala
 475 480

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<211> 468

<212> PRT

<213> Homo sapiens

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 35 40 45

His His Ala Arg Arg Gly Pro Arg Gly Ser Leu Arg Gly Pro Pro Pro
 50 55 60

Pro Pro Thr Ala His Glu Glu Leu Gly Thr Ala Ala Ala Ala Ala
 65 70 75 80

Ala Ala Ser Arg Ser Ala Met Val Thr Ser Met Ala Ser Ile Leu Asp
 85 90

Gly Gly Asp Tyr Arg Pro Glu Leu Ser Ile Pro Leu His His Ala Met
 100 105 110

Ser Met Ser Cys Asp Ser Ser Thr Pro Pro Gly Met Gly Met Ser Asn Thr
 115 120 125
 Tyr Thr Leu Thr Pro Leu Glu Pro Leu Pro Pro Ile Ser Thr Val
 130 135 140
 Ser Asp Lys Phe His His Pro His His His Pro His His His His
 145 150 155 160
 His His His His His Glu Arg Leu Ser Gly Asn Val Ser Gly Ser Phe
 165 170 175
 Thr Leu Met Arg Asp Glu Arg Gly Leu Pro Ala Met Asn Asn Leu Tyr
 180 185 190
 Ser Pro Tyr Lys Glu Met Pro Gly Met Ser Glu Ser Leu Ser Pro Leu
 195 200 205
 Ala Ala Thr Pro Leu Gly Asn Gly Leu Gly Gly Leu His Asn Ala Glu
 210 215 220
 Glu Ser Leu Pro Asn Tyr Gly Pro Pro Gly His Asp Lys Met Leu Ser
 225 230 235 240
 Pro Asn Phe Asp Ala His His Thr Ala Met Leu Thr Arg Gly Glu Glu
 245 250 255
 His Leu Ser Arg Gly Leu Gly Thr Pro Pro Ala Ala Met Met Ser His
 260 265 270
 Leu Asn Gly Leu His His Pro Gly His Thr Glu Ser His Gly Pro Val
 275 280 285
 Leu Ala Pro Ser Arg Glu Arg Pro Pro Ser Ser Ser Ser Gly Ser Glu
 290 295 300
 Val Ala Thr Ser Gly Glu Leu Glu Ile Asn Thr Lys Glu Val Ala
 305 310 320
 Glu Arg Ile Thr Ala Glu Leu Lys Arg Tyr Ser Ile Pro Glu Ala Ile
 325 330 335
 Phe Ala Glu Arg Val Leu Cys Arg Ser Glu Gly Thr Leu Ser Asp Leu
 340 345 350
 Leu Arg Asn Pro Lys Pro Trp Ser Lys Leu Lys Ser Gly Arg Glu Thr
 355 360 365
 Phe Arg Arg Met Trp Lys Trp Leu Glu Pro Glu Phe Glu Arg Met
 370 375 380
 Ser Ala Leu Arg Leu Ala Ala Cys Lys Arg Lys Glu Glu Glu Pro Asn
 385 390 395 400
 Lys Asp Arg Asn Asn Ser Glu Lys Lys Ser Arg Leu Val Phe Thr Asp
 405 410 415
 Leu Glu Arg Arg Thr Leu Phe Ala Ile Phe Lys Glu Asn Lys Arg Pro
 420 425 430

ser lys 311 Met 312 Ile 313 Thr 314 Ser 315 Glu 316 Leu 317 Ile 318
Ser 319 Ile 320 Asp 321 Ile 322 Ser 323 Glu 324 Leu 325 Ile 326
Ser 327 Ile 328 Asp 329 Ile 330 Ser 331 Glu 332 Leu 333 Ile 334

Thr Thr Val Ser Asn Ser Phe Met Asn Ala Arg Arg Arg Ser Leu Glu
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lys Cys Glu Asp Asp Leu Ser Thr Gly Gly Ser Ser Ser Thr Ser Ser
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<212> DNA

<213> *Homo sapiens*

4220

42018-023

<002> (1) . (1463)

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Arg Gly Glu Leu Ala Gly Pro Leu His Pro Ala Met Gly Met Ala Cys
Arg Gly Glu Leu Ala Gly Pro Leu His Pro Ala Met Gly Met Ala Cys
85 90 95

33
Gly Ala Pro Gly Leu Gly Gly Thr Tyr Thr Thr Leu Thr Pro Leu Glu
34 35 36 37 38 39 40 41 42 43 44 45 46 47 48 49 50 51 52 53 54 55 56 57 58 59 60 61 62 63 64 65 66 67 68 69 70 71 72 73 74 75 76 77 78 79 80 81 82 83 84 85 86 87 88 89 90 91 92 93 94 95 96 97 98 99 100

360	138	400
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Arg Lys Glu Glu Glu Glu Lys Glu Asp Ala Leu Glu Pro Lys Lys 415		
405		
caq cgt ctc gtc acc dac ctc caq cga cgg acc ctc atc gco atc Gln Arg Leu Val Phe Thr Asp Leu Glu Arg Arg Thr Leu Ile Ala Ile 420		11296
420		
ccg aag gaa aac aag cgg ctc aag gaa atg caq gtc acc atc tcc Phe Lys Glu Asn Lys Arg Pro Ser Lys Glu Met Glu Val Thr Ile Ser 445		13444
Phe Lys Glu Asn Lys Arg Pro Ser Lys Glu Met Glu Val Thr Ile Ser 445		
435		
caq cag ctc ggc ttc gag ctc aac acc gtc agc aac ttc ttc atg aac Gln Leu Glu Leu Glu Leu Asn Thr Val Ser Asn Phe Phe Met Asn 460		1392
Gln Leu Glu Leu Glu Leu Asn Thr Val Ser Asn Phe Phe Met Asn 460		
450		
ggc cgg cgt cgc tgg arg aac cgg tgg cct caq gaa ccc agc acc gcc Ala Arg Arg Arg Cys Met Asn Arg Trp Ala Glu Glu Pro Ser Thr Ala 475		14440
Ala Arg Arg Arg Cys Met Asn Arg Trp Ala Glu Glu Pro Ser Thr Ala 475		
465		
ccg ggc ggc acc ggc ggc acc acc ttc tcc aag gcc tgg Pro Glu Glu Pro Ala Glu Ala Thr Ala Thr Ser Lys Ala 485		14285
Pro Glu Glu Pro Ala Glu Ala Thr Ala Thr Ser Lys Ala 485		

146 160 165 160
 Ala Ala Ser Val Ser Gly Ser Phe Thr Leu Met Arg Asp Glu Arg Ala
 166 170 175 175
 Ala Leu Ala Ser Val Gly His Leu Tyr Gly Pro Tyr Gly Lys Glu Leu
 180 185 190 190
 Pro Ala Met Gly Ser Pro Leu Ser Pro Leu Pro Asn Ala Leu Pro Pro
 195 200 205 205
 Ala Leu His Gly Ala Pro Glu Pro Pro Pro Pro Pro Pro Pro Pro Pro
 210 215 220 220
 Leu Ala Ala Tyr Gly Pro Pro Gly His Leu Ala Gly Asp Lys Leu Leu
 225 230 235 240
 Pro Pro Ala Ala Phe Glu Pro His Ala Ala Leu Leu Gly Arg Ala Glu
 245 250 255 255
 Asp Ala Leu Ala Arg Gly Leu Pro Gly Gly Gly Thr Gly Ser
 260 265 270 270
 Gly Gly Ala Gly Ser Gly Ser Ala Ala Gly Leu Leu Ala Pro Leu Gly
 275 280 285 290
 Gly Leu Ala Ala Ala Gly Ala His Gly Pro His Gly Gly Gly Gly
 295 300 305 310
 Pro Gly Gly Ser Gly Gly Pro Ser Ala Gly Ala Ala Ala Glu Glu
 315 320 325 325
 Ile Asn Thr Lys Glu Val Ala Glu Arg Ile Thr Ala Glu Leu Lys Arg
 330 335 335 335
 Tyr Ser Ile Pro Glu Ala Ile Phe Ala Glu Arg Ile Leu Cys Arg Ser
 340 345 350 350
 Glu Gly Thr Leu Ser Asp Leu Leu Arg Asn Pro Lys Pro Trp Ser Lys
 355 360 365 365
 Leu Lys Ser Gly Arg Glu Thr Phe Arg Arg Met Trp Lys Trp Leu Glu
 370 375 380 380
 Glu Pro Glu Phe Glu Arg Met Ser Ala Leu Arg Leu Ala Ala Cys Lys
 390 395 400 400
 Arg Lys Glu Glu Glu Glu Lys Glu Arg Ala Leu Glu Pro Lys Lys
 405 410 415 415
 Glu Arg Leu Val Phe Thr Asp Leu Glu Arg Arg Thr Leu Ile Ala Ile
 420 425 430 430
 Phe Lys Glu Asn Lys Arg Pro Ser Lys Glu Met Glu Val Thr Ile Ser
 435 440 445 445
 Glu Glu Leu Gly Leu Glu Leu Asn Thr Val Ser Asn Phe Phe Met Asn
 450 455 460 460
 Ala Arg Arg Arg Cys Met Asn Arg Trp Ala Glu Glu Pro Ser Thr Ala
 465 470 475 475
 475 480 480

Pro City City Pro Ala City Ala Thor Ala Thor Phe Ser Lys Ala
485 490